

24. The method of Claim 23, wherein said essential amino acids are selected from the group consisting of methionine, tryptophan, lysine, valine, phenylalanine, isoleucine, leucine, threonine and cysteine.

25. The method of Claim 23, wherein said amino acid changes comprise increasing the levels of methionine.

26. The method of Claim 23, wherein said amino acid changes are introduced into predetermined sites.

27. The method of Claim 26, wherein said predetermined sites are determined by secondary structure prediction or homology comparison.

28. The method of Claim 23, wherein said amino acid changes are introduced at random.

29. The method of Claim 28, wherein said amino acid changes are produced by mutagenic PCR, DNA shuffling, or phage display methodology.

30. The method of Claim 29, wherein correctly folded variants are confirmed by filter lift assay or ELISA.

31. The method of Claim 23, wherein said essential amino acids are increased to represent 5% of the total amino acid content of the protein.

32. The method of Claim 23, wherein said essential amino acids are increased to represent 10% of the total amino acid content of the protein.

33. The method of Claim 23, wherein said protein is vegetative storage protein.

34. An engineered protein having altered amino acid composition, wherein said amino acid composition has been altered by introducing amino acid changes into said protein, wherein said engineered protein binds to a set of interacting molecules capable of binding with a corresponding native protein, and wherein said molecules recognize native conformation.

35. The protein of claim 34, wherein said protein is selected from the group consisting of:

- a) a protein having the amino acid sequence set forth in SEQ ID NO: 8;
- b) a protein having the amino acid sequence set forth in SEQ ID NO: 9; and
- c) a protein having the amino acid sequence set forth in SEQ ID NO: 10.

36. The protein of claim 35, wherein said protein has the amino acid sequence set forth in SEQ ID NO: 8.

37. The protein of Claim 34, wherein said interacting molecules are antibodies.

38. The protein of Claim 37, wherein said antibodies are monoclonal antibodies.

39. The protein of Claim 34, wherein said amino acid changes increase the levels of at least one essential amino acid in the protein.

40. The protein of Claim 39, wherein said essential amino acids are selected from the group consisting of methionine, tryptophan, lysine, valine, phenylalanine, isoleucine, leucine, threonine and cysteine.

41. The protein of Claim 40, wherein said essential amino acids are increased to represent 5% of the total amino acid content of the protein.

42. The protein of Claim 39, wherein said essential amino acids are increased to represent 10% of the total amino acid content of the protein.

43. The protein of claim 39, wherein said amino acid changes increase the level of methionine.

44. The protein of Claim 34, wherein said amino acid changes are introduced into predetermined sites.

45. The protein of Claim 44 wherein said predetermined sites are determined by secondary structure prediction or homology comparison.

46. The protein of Claim 34, wherein said amino acid changes are introduced at random.

47. The protein of Claim 46, wherein said amino acid changes are produced by mutagenic PCR, DNA shuffling, or phage display methodology.

48. The protein of Claim 34, wherein said protein is vegetative storage protein.

49. An engineered vegetative storage protein having altered amino acid composition, wherein said amino acid composition has been altered by introducing amino acid changes into said protein, wherein said protein binds to a set of monoclonal antibodies capable of binding with a corresponding native vegetative storage protein, and wherein said antibodies recognize native conformation.